

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/192,861DATE: 04/21/94
TIME: 09:55:38

INPUT SET: S2032.raw

This Raw Listing contains only the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

ENTERED

(1) General Information:

(i) APPLICANT: Le, Junming
Vilcek, Jan
Daddona, Peter E.
Ghrayeb, John
Knight, David M.
Siegel, Scott A.

(ii) TITLE OF INVENTION: ANTI-TNF ANTIBODIES AND PEPTIDES
OF HUMAN TUMOR NECROSIS FACTOR

(iii) NUMBER OF SEQUENCES: 19

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Browdy and Neimark
(B) STREET: 419 Seventh Street, N.W.
(C) CITY: Washington
(D) STATE: D.C.
(E) COUNTRY: USA
(F) ZIP: 20004

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/192,861
(B) FILING DATE: 04-FEB-1994

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/013,413
(B) FILING DATE: 02-FEB-1993

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/010,406
(B) FILING DATE: 29-JAN-1993

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 07/943,852
(B) FILING DATE: 11-SEP-1992

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/192,861DATE: 04/21/94
TIME: 09:55:43

INPUT SET: S2032.raw

47 (vii) PRIOR APPLICATION DATA:
48 (A) APPLICATION NUMBER: US 07/853,606
49 (B) FILING DATE: 18-MAR-1992
50
51 (vii) PRIOR APPLICATION DATA:
52 (A) APPLICATION NUMBER: US 07/670,827
53 (B) FILING DATE: 18-MAR-1991
54
55 (viii) ATTORNEY/AGENT INFORMATION:
56 (A) NAME: TOWNSEND, G. Kevin
57 (B) REGISTRATION NUMBER: 34,033
58 (C) REFERENCE/DOCKET NUMBER: LE1/VILCEK=3E
59
60 (ix) TELECOMMUNICATION INFORMATION:
61 (A) TELEPHONE: 202-628-5197
62 (B) TELEFAX: 202-737-3528
63
64
65 (2) INFORMATION FOR SEQ ID NO:1:
66
67 (i) SEQUENCE CHARACTERISTICS:
68 (A) LENGTH: 157 amino acids
69 (B) TYPE: amino acid
70 (D) TOPOLOGY: linear
71
72 (ii) MOLECULE TYPE: peptide
73
74 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
75
76 Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His Val
77 1 5 10 15
78
79 Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg
80 20 25 30
81
82 Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu
83 35 40 45
84
85 Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe
86 50 55 60
87
88 Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile
89 65 70 75 80
90
91 Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala
92 85 90 95
93
94 Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys
95 100 105 110
96
97 Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys
98 115 120 125
99

RAW SEQUENCE LISTING PATENT APPLICATION US/08/192,861

DATE: 04/21/94
TIME: 09:55:49

INPUT SET: S2032.raw

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100      Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe
101          130                      135                      140
102
103      Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu
104          145                      150                      155
105
106
107 (2) INFORMATION FOR SEQ ID NO:2:
108
109      (i) SEQUENCE CHARACTERISTICS:
110          (A) LENGTH: 321 base pairs
111          (B) TYPE: nucleic acid
112          (C) STRANDEDNESS: single
113          (D) TOPOLOGY: linear
114
115      (ii) MOLECULE TYPE: cDNA
116
117
118      (ix) FEATURE:
119          (A) NAME/KEY: CDS
120          (B) LOCATION: 1..321
121
122
123      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
124
125      GAC ATC TTG CTG ACT CAG TCT CCA GCC ATC CTG TCT GTG AGT CCA GGA      48
126      Asp Ile Leu Leu Thr Gln Ser Pro Ala Ile Leu Ser Val Ser Pro Gly
127          1                      5                      10                      15
128
129      GAA AGA GTC AGT TTC TCC TGC AGG GCC AGT CAG TTC GTT GGC TCA AGC      96
130      Glu Arg Val Ser Phe Ser Cys Arg Ala Ser Gln Phe Val Gly Ser Ser
131          20                      25                      30
132
133      ATC CAC TGG TAT CAG CAA AGA ACA AAT GGT TCT CCA AGG CTT CTC ATA      144
134      Ile His Trp Tyr Gln Gln Arg Thr Asn Gly Ser Pro Arg Leu Leu Ile
135          35                      40                      45
136
137      AAG TAT GCT TCT GAG TCT ATG TCT GGG ATC CCT TCC AGG TTT AGT GGC      192
138      Lys Tyr Ala Ser Glu Ser Met Ser Gly Ile Pro Ser Arg Phe Ser Gly
139          50                      55                      60
140
141      AGT GGA TCA GGG ACA GAT TTT ACT CTT AGC ATC AAC ACT GTG GAG TCT      240
142      Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Asn Thr Val Glu Ser
143          65                      70                      75                      80
144
145      GAA GAT ATT GCA GAT TAT TAC TGT CAA CAA AGT CAT AGC TGG CCA TTC      288
146      Glu Asp Ile Ala Asp Tyr Tyr Cys Gln Gln Ser His Ser Trp Pro Phe
147          85                      90                      95
148
149      ACG TTC GGC TCG GGG ACA AAT TTG GAA GTA AAA                        321
150      Thr Phe Gly Ser Gly Thr Asn Leu Glu Val Lys
151          100                      105
152

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RAW SEQUENCE LISTING
PATENT APPLICATION US/08/192,861DATE: 04/21/94
TIME: 09:55:54

INPUT SET: S2032.raw

153
154 (2) INFORMATION FOR SEQ ID NO:3:
155
156 (i) SEQUENCE CHARACTERISTICS:
157 (A) LENGTH: 107 amino acids
158 (B) TYPE: amino acid
159 (D) TOPOLOGY: linear
160
161 (ii) MOLECULE TYPE: protein
162
163 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
164
165 Asp Ile Leu Leu Thr Gln Ser Pro Ala Ile Leu Ser Val Ser Pro Gly
166 1 5 10 15
167
168 Glu Arg Val Ser Phe Ser Cys Arg Ala Ser Gln Phe Val Gly Ser Ser
169 20 25 30
170
171 Ile His Trp Tyr Gln Gln Arg Thr Asn Gly Ser Pro Arg Leu Leu Ile
172 35 40 45
173
174 Lys Tyr Ala Ser Glu Ser Met Ser Gly Ile Pro Ser Arg Phe Ser Gly
175 50 55 60
176
177 Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Asn Thr Val Glu Ser
178 65 70 75 80
179
180 Glu Asp Ile Ala Asp Tyr Tyr Cys Gln Gln Ser His Ser Trp Pro Phe
181 85 90 95
182
183 Thr Phe Gly Ser Gly Thr Asn Leu Glu Val Lys
184 100 105
185
186 (2) INFORMATION FOR SEQ ID NO:4:
187
188 (i) SEQUENCE CHARACTERISTICS:
189 (A) LENGTH: 357 base pairs
190 (B) TYPE: nucleic acid
191 (C) STRANDEDNESS: single
192 (D) TOPOLOGY: linear
193
194 (ii) MOLECULE TYPE: cDNA
195
196
197 (ix) FEATURE:
198 (A) NAME/KEY: CDS
199 (B) LOCATION: 1..357
200
201
202 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
203
204 GAA GTG AAG CTT GAG GAG TCT GGA GGA GGC TTG GTG CAA CCT GGA GGA 48
205 Glu Val Lys Leu Glu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

RAW SEQUENCE LISTING PATENT APPLICATION US/08/192,861

DATE: 04/21/94
TIME: 09:56:00

INPUT SET: S2032.raw

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206      1          5          10          15
207
208   TCC ATG AAA CTC TCC TGT GTT GCC TCT GGA TTC ATT TTC AGT AAC CAC   96
209   Ser Met Lys Leu Ser Cys Val Ala Ser Gly Phe Ile Phe Ser Asn His
210                20                25                30
211
212   TGG ATG AAC TGG GTC CGC CAG TCT CCA GAG AAG GGG CTT GAG TGG GTT   144
213   Trp Met Asn Trp Val Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Val
214                35                40                45
215
216   GCT GAA ATT AGA TCA AAA TCT ATT AAT TCT GCA ACA CAT TAT GCG GAG   192
217   Ala Glu Ile Arg Ser Lys Ser Ile Asn Ser Ala Thr His Tyr Ala Glu
218                50                55                60
219
220   TCT GTG AAA GGG AGG TTC ACC ATC TCA AGA GAT GAT TCC AAA AGT GCT   240
221   Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ala
222                65                70                75                80
223
224   GTC TAC CTG CAA ATG ACC GAC TTA AGA ACT GAA GAC ACT GGC GTT TAT   288
225   Val Tyr Leu Gln Met Thr Asp Leu Arg Thr Glu Asp Thr Gly Val Tyr
226                85                90                95
227
228
229
230   TAC TGT TCC AGG AAT TAC TAC GGT AGT ACC TAC GAC TAC TGG GGC CAA   336
231   Tyr Cys Ser Arg Asn Tyr Tyr Gly Ser Thr Tyr Asp Tyr Trp Gly Gln
232                100                105                110
233
234   GGC ACC ACT CTC ACA GTC TCC                                     357
235   Gly Thr Thr Leu Thr Val Ser
236                115
237
238
239   (2) INFORMATION FOR SEQ ID NO:5:
240
241       (i) SEQUENCE CHARACTERISTICS:
242           (A) LENGTH: 119 amino acids
243           (B) TYPE: amino acid
244           (D) TOPOLOGY: linear
245
246       (ii) MOLECULE TYPE: protein
247
248       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
249
250   Glu Val Lys Leu Glu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
251      1          5          10          15
252
253   Ser Met Lys Leu Ser Cys Val Ala Ser Gly Phe Ile Phe Ser Asn His
254                20                25                30
255
256   Trp Met Asn Trp Val Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Val
257                35                40                45
258

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PAGE: 1

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/08/192,861

DATE: 04/21/94
TIME: 09:56:05

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